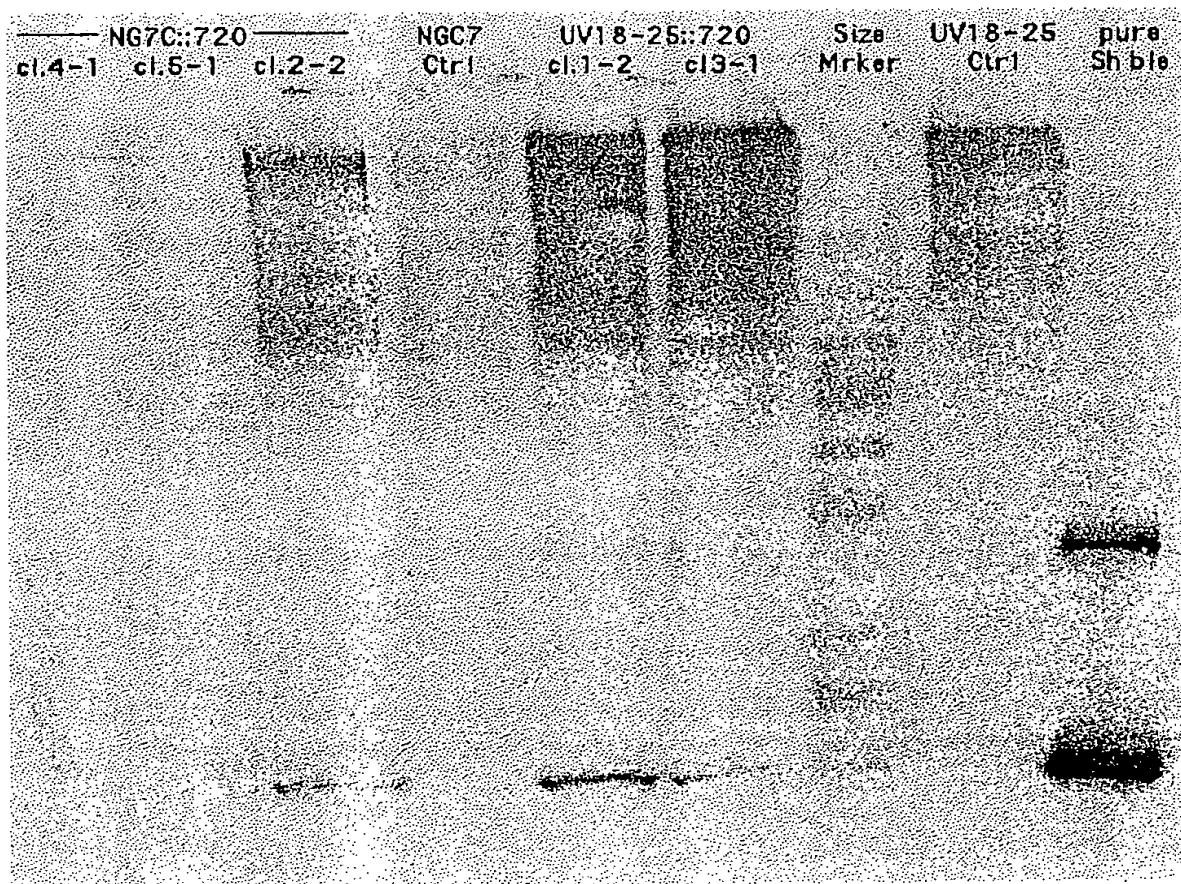


Fig 1



09334430

Fig 2

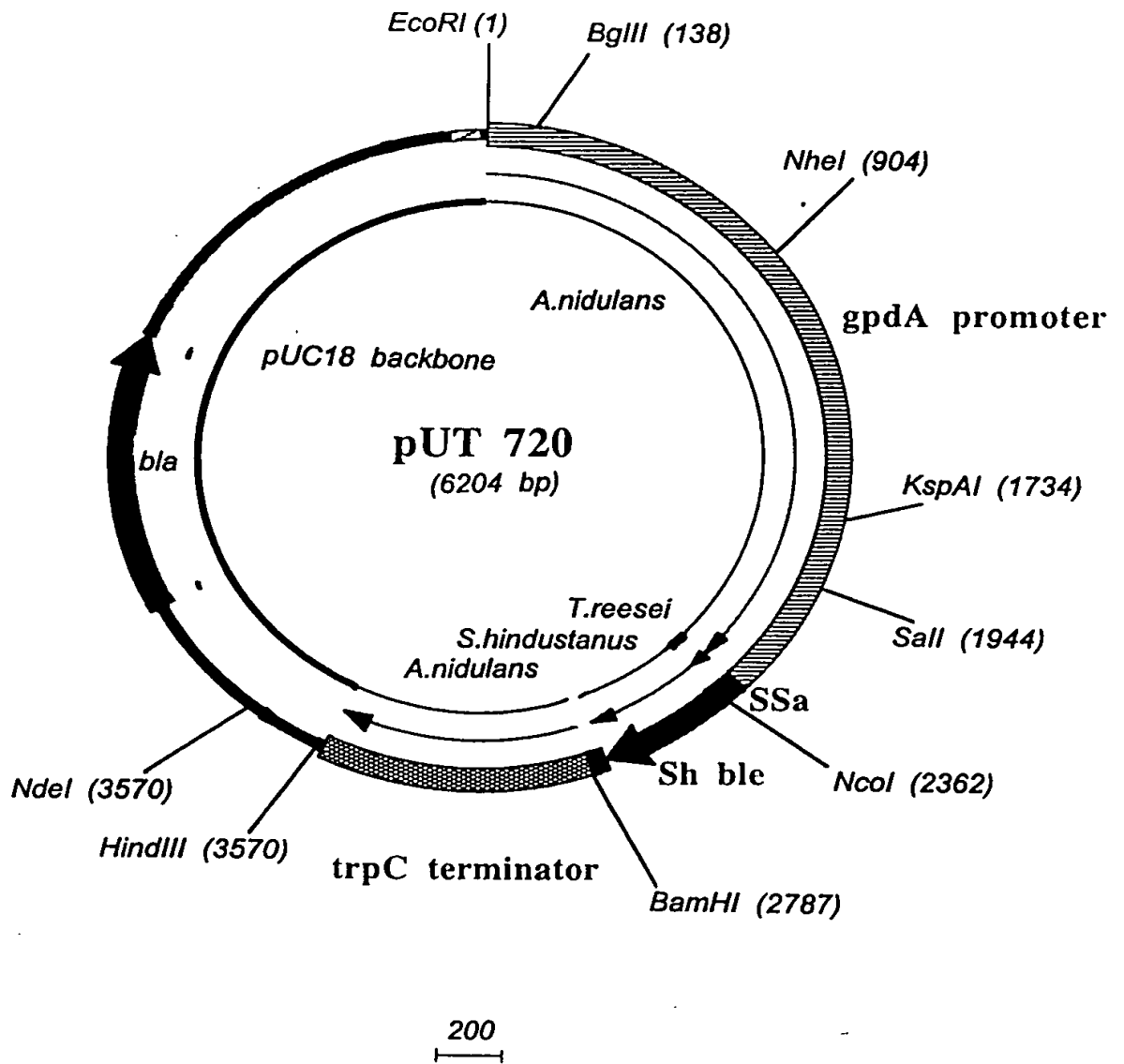
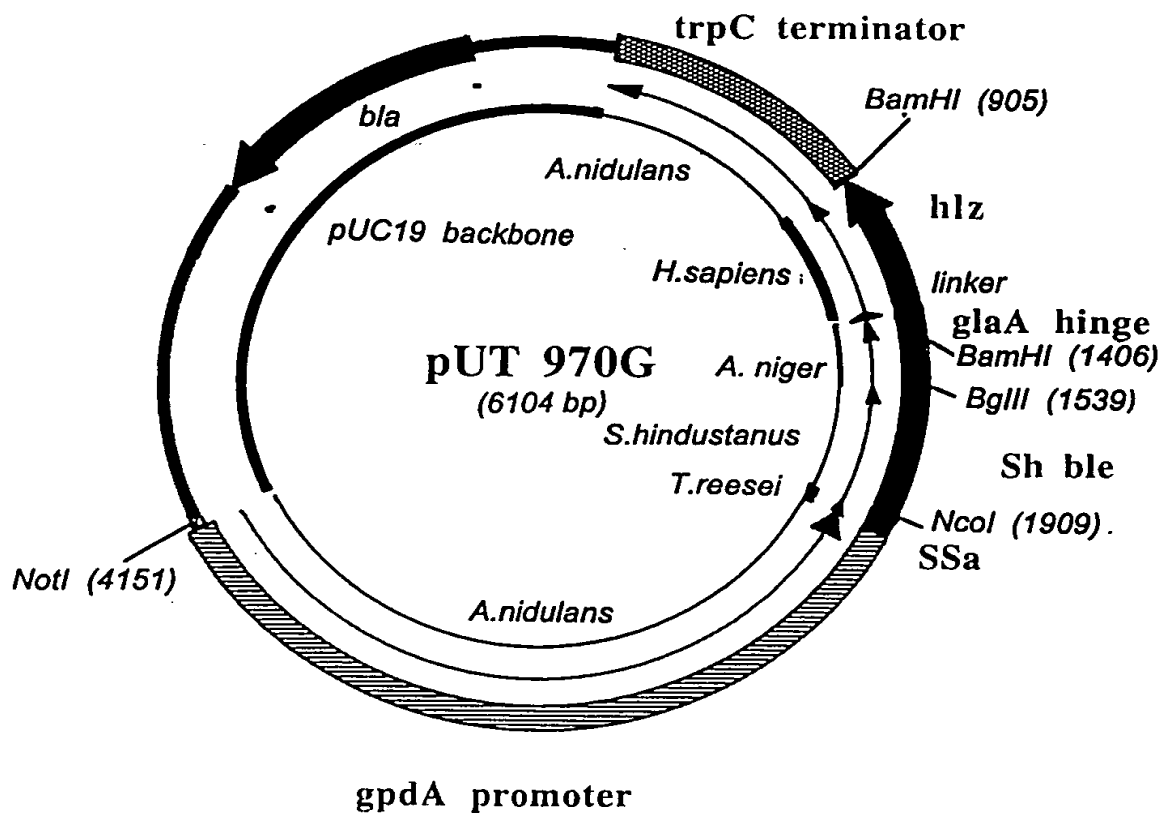


Fig 3



200



Fig 4

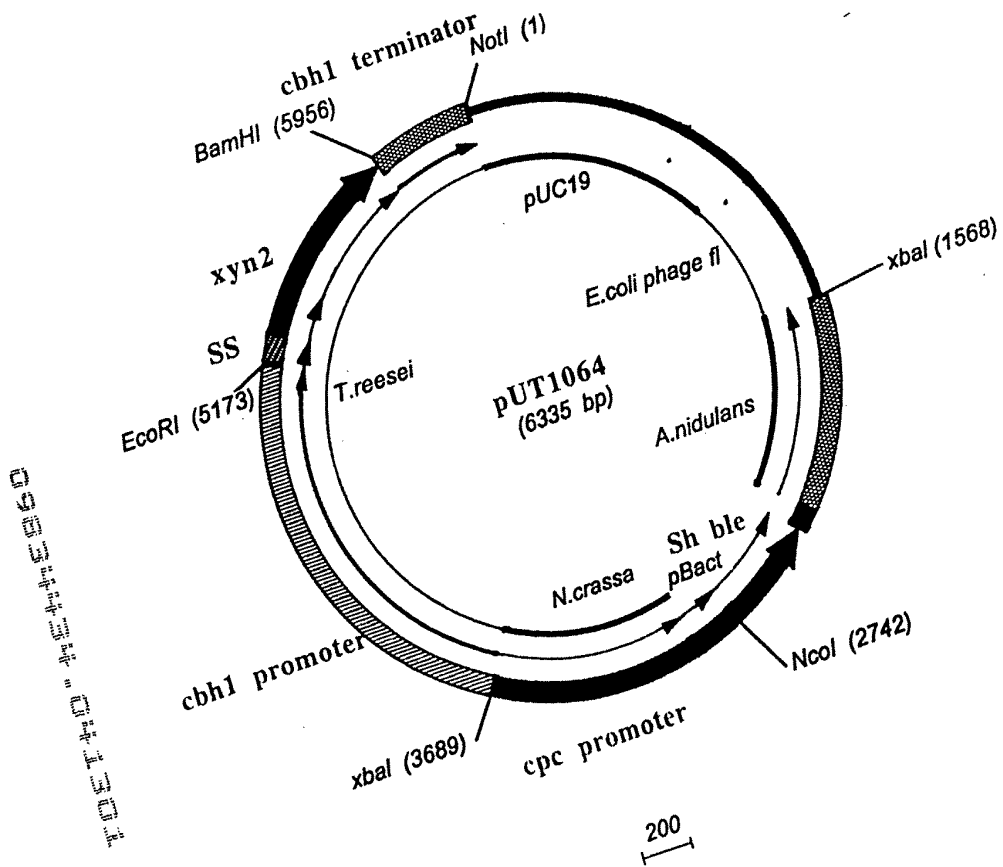
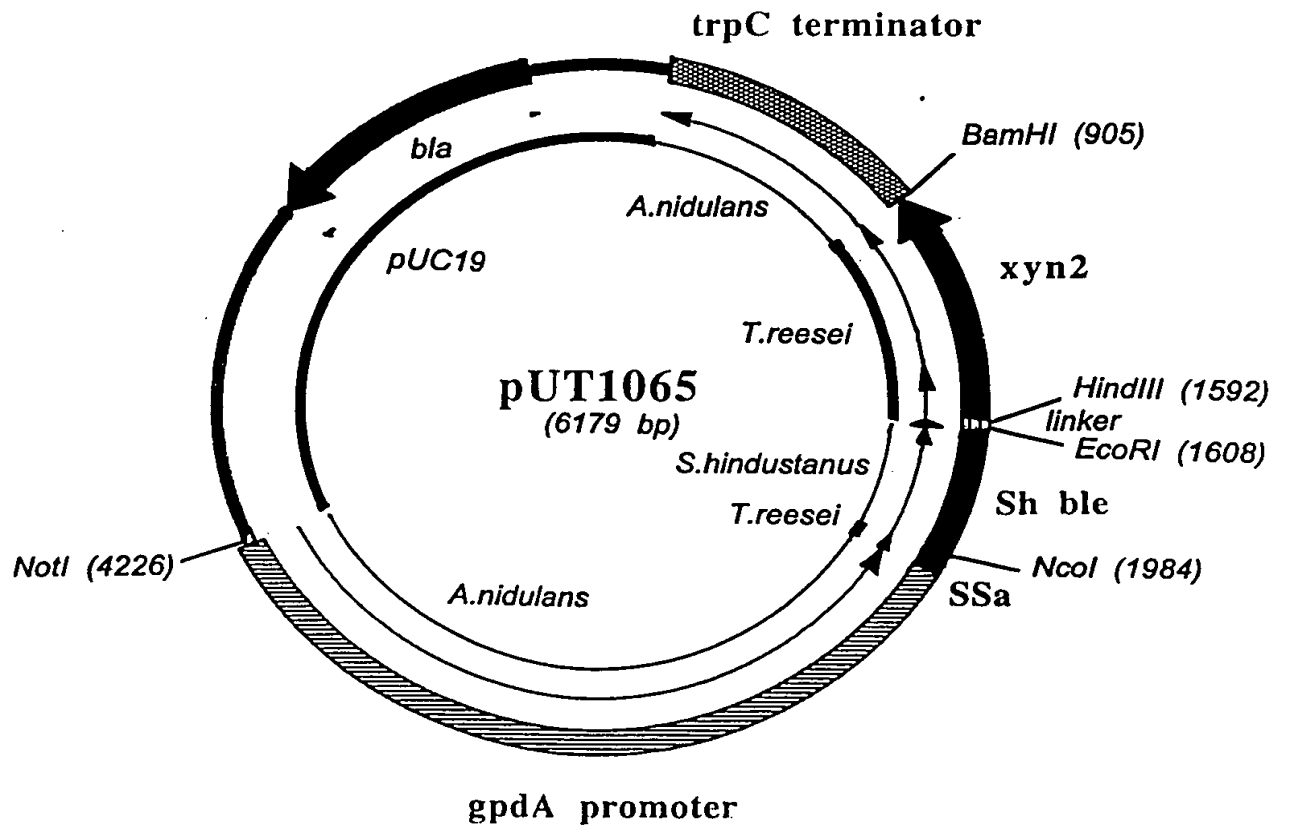


Fig 5



200

Fig 6

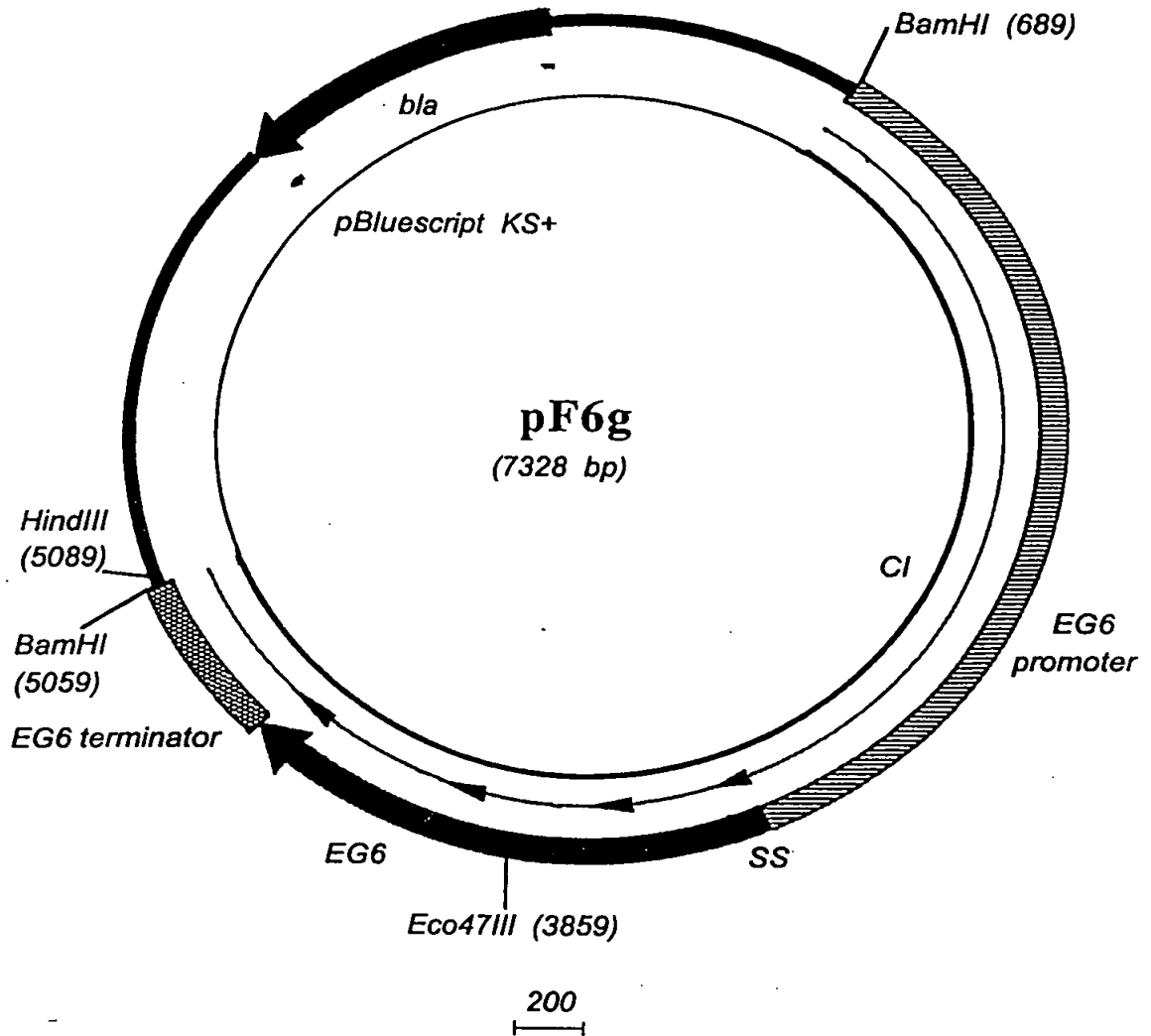
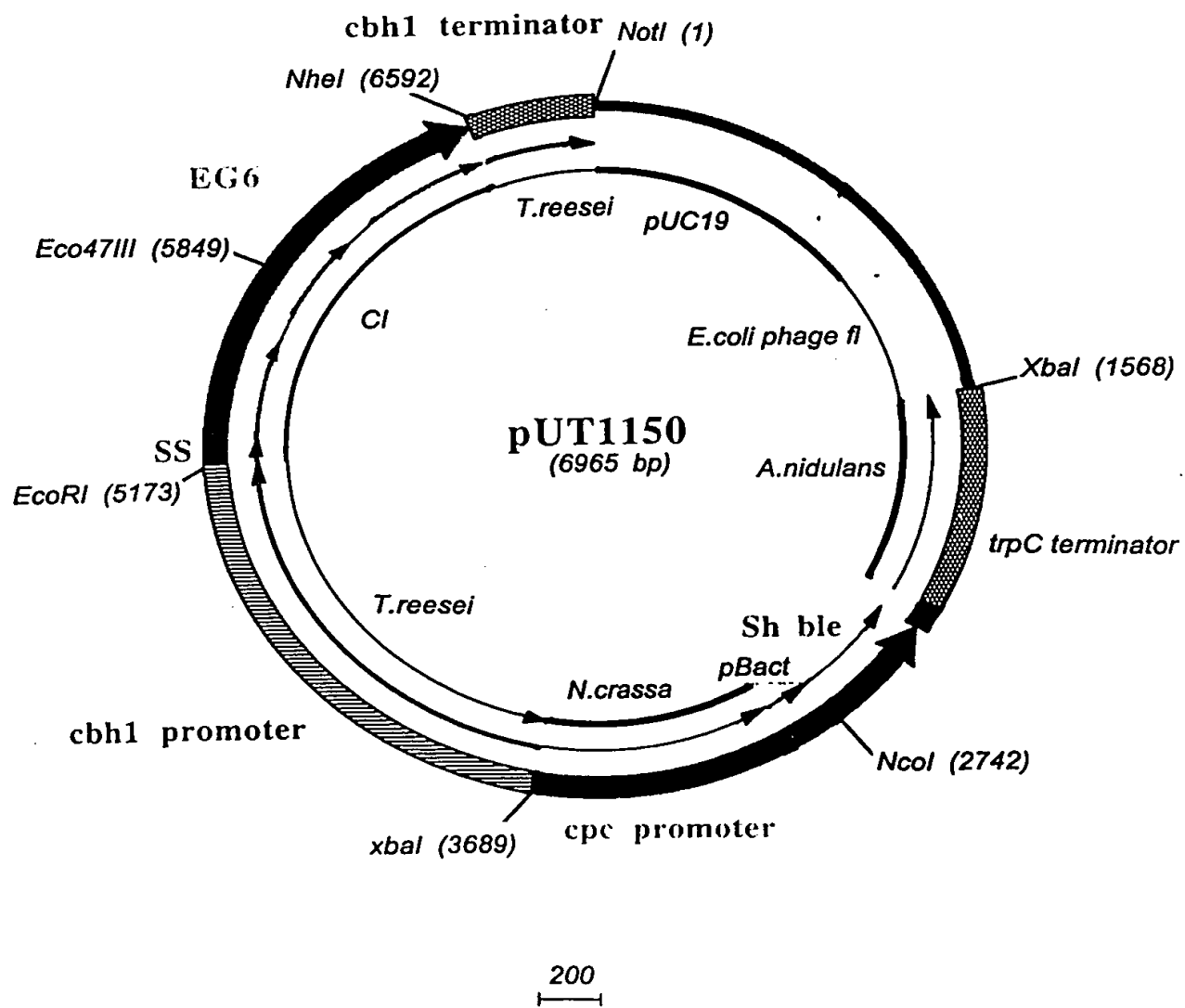
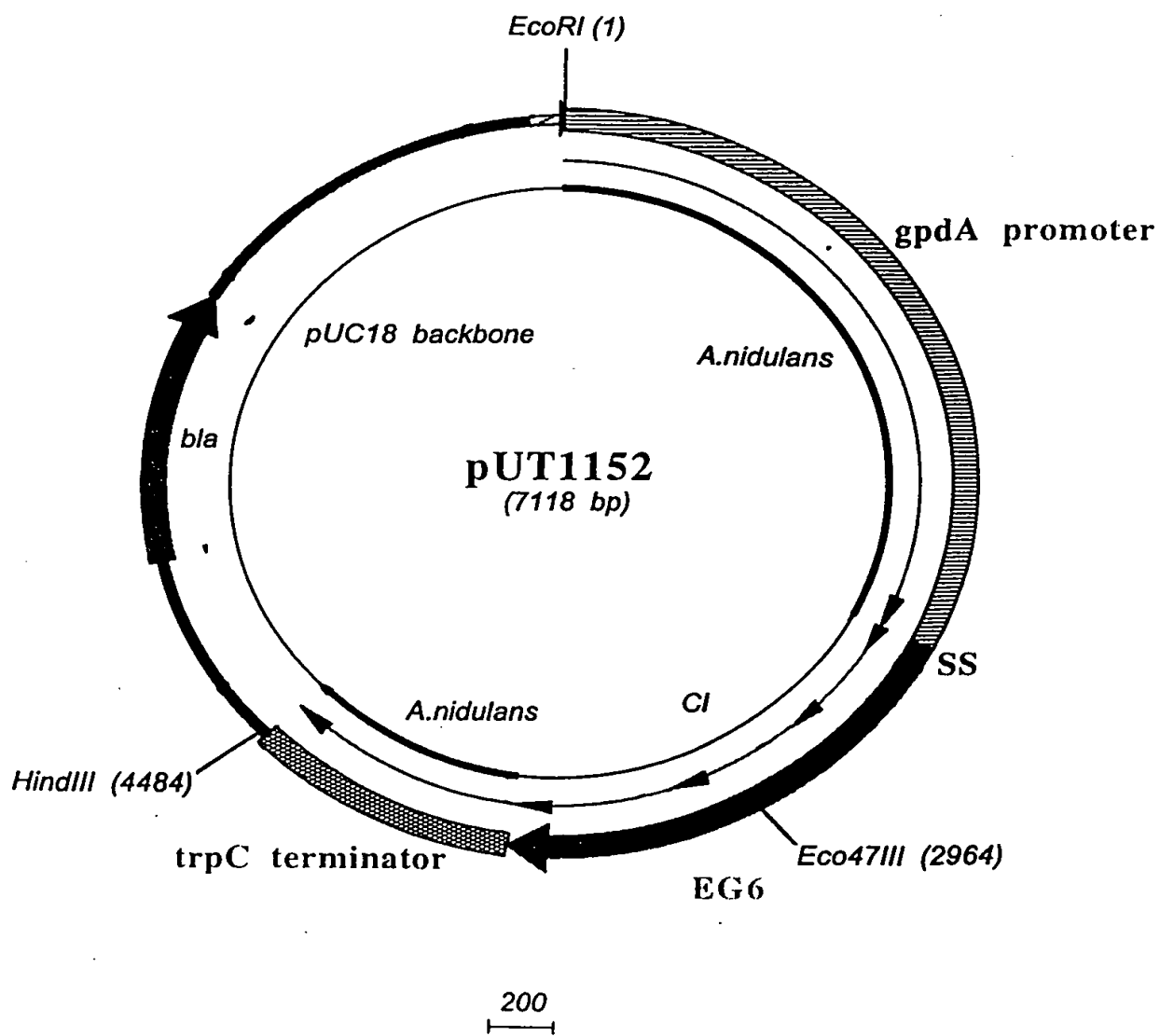


Fig 7



09444-44444

Fig 8



033440401

Fig 9

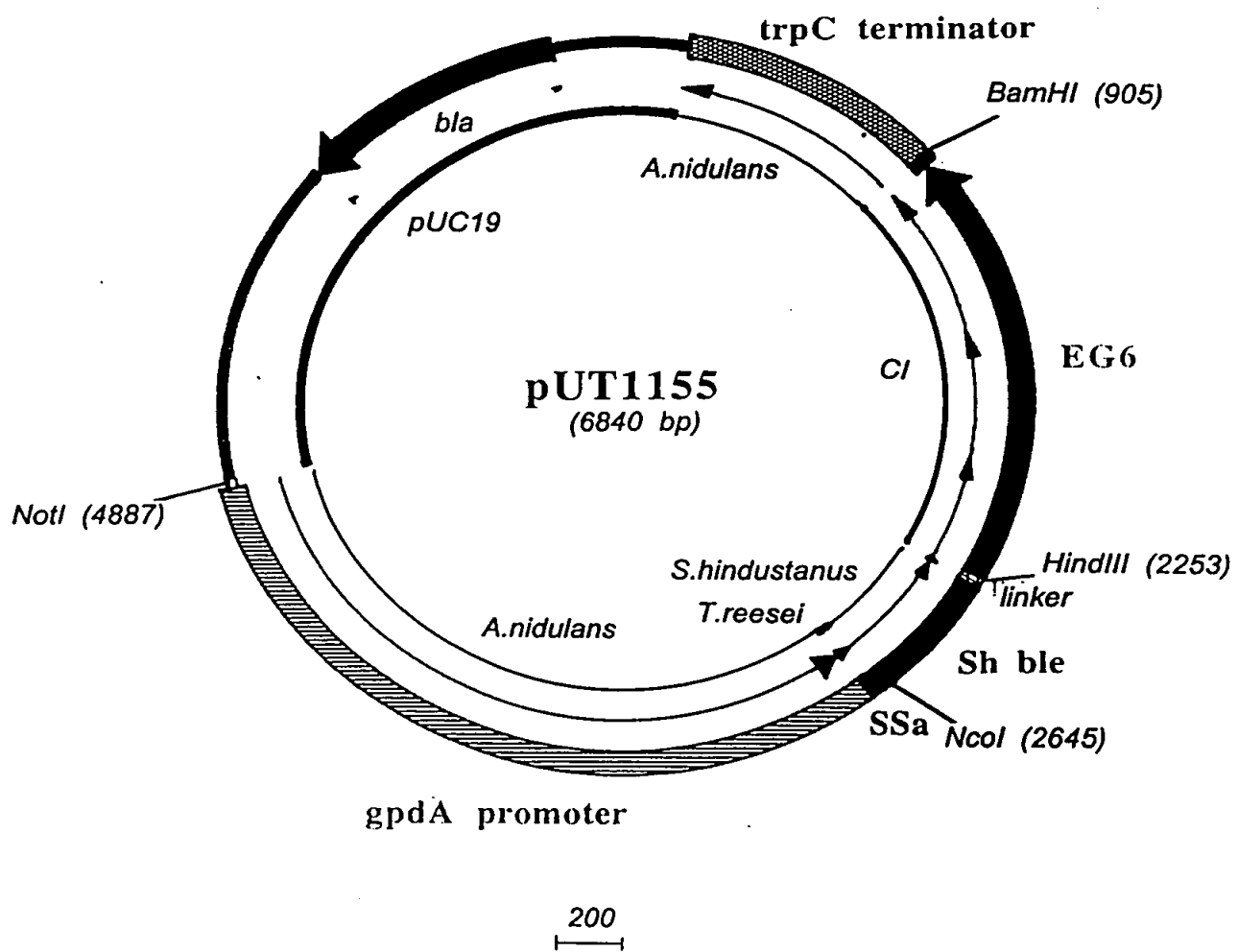
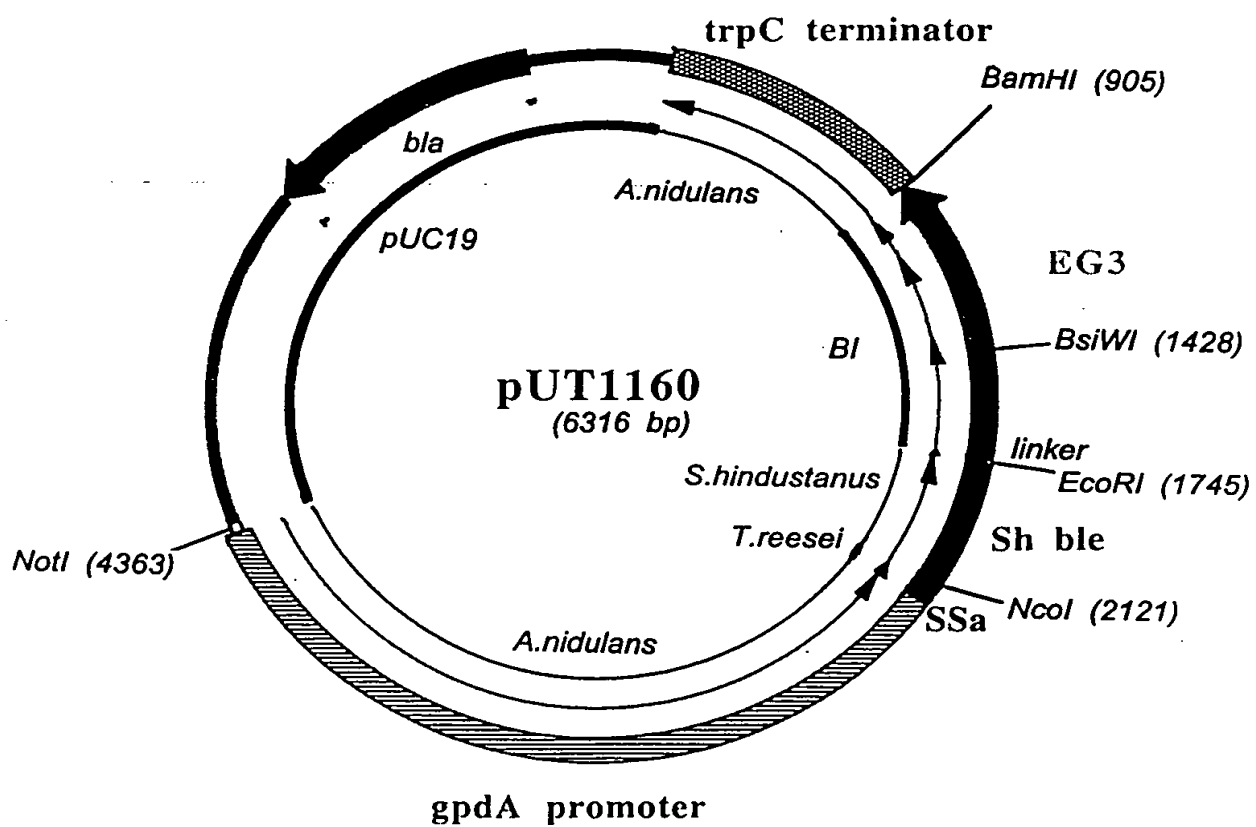


Fig 10

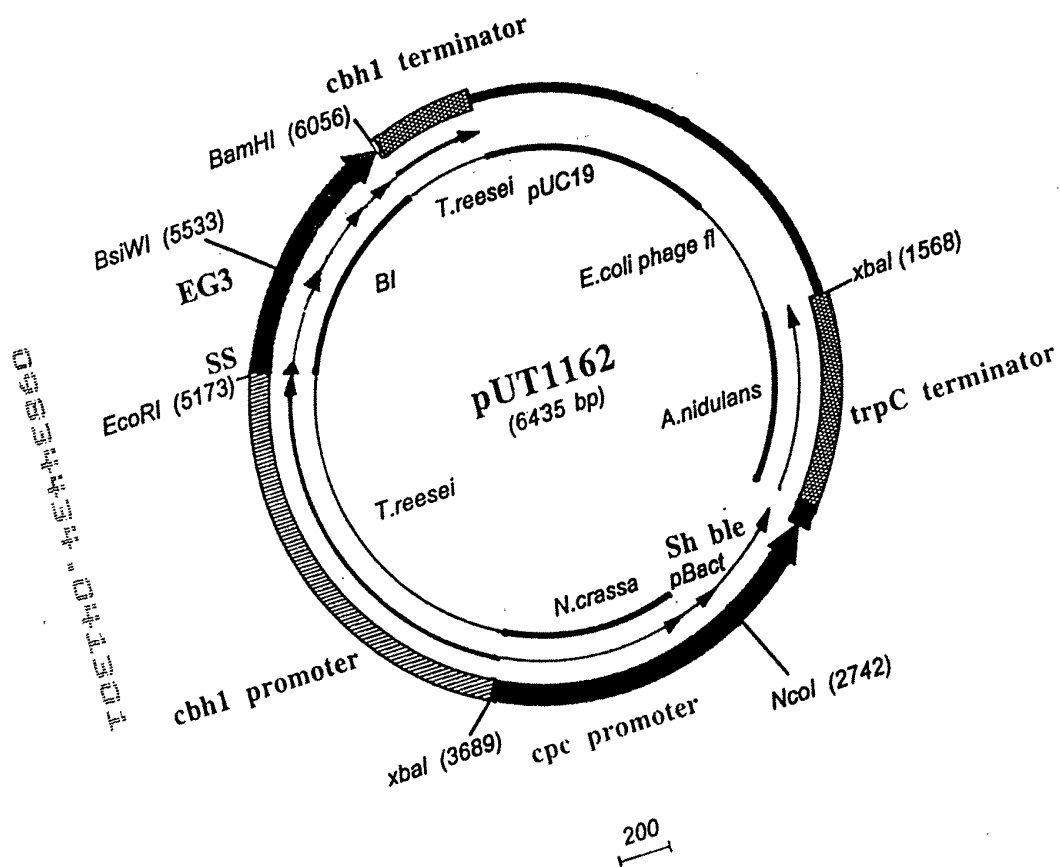


200



03634434 041304 706740 4445850

Fig 11



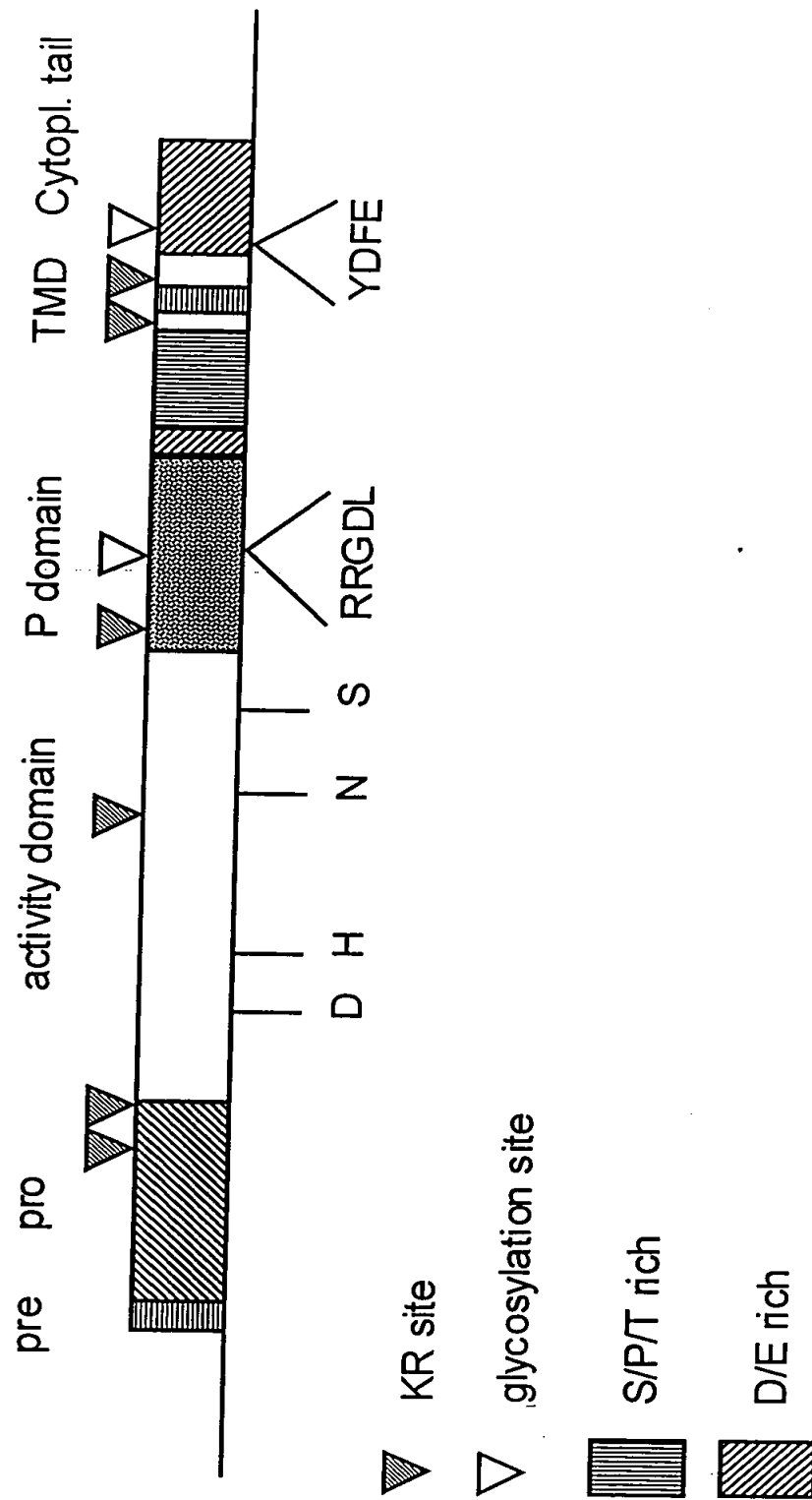


Fig 12

FOET40" 4E44E850

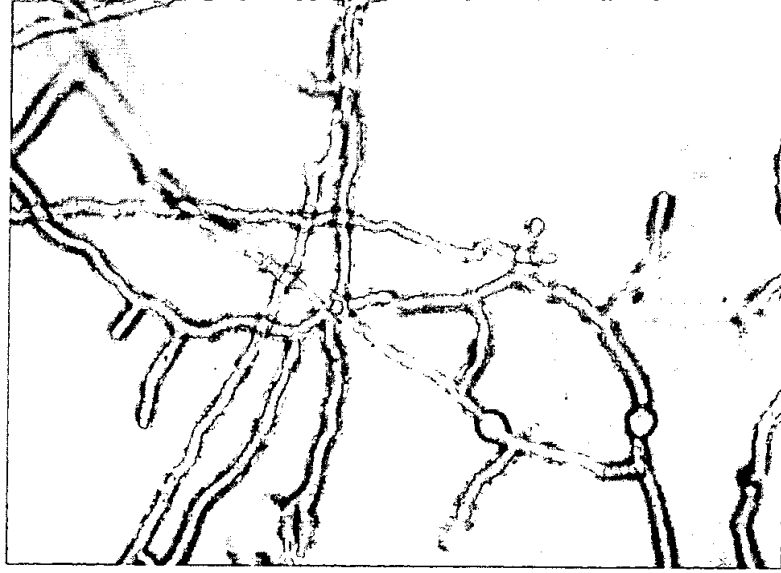


Fig 13A

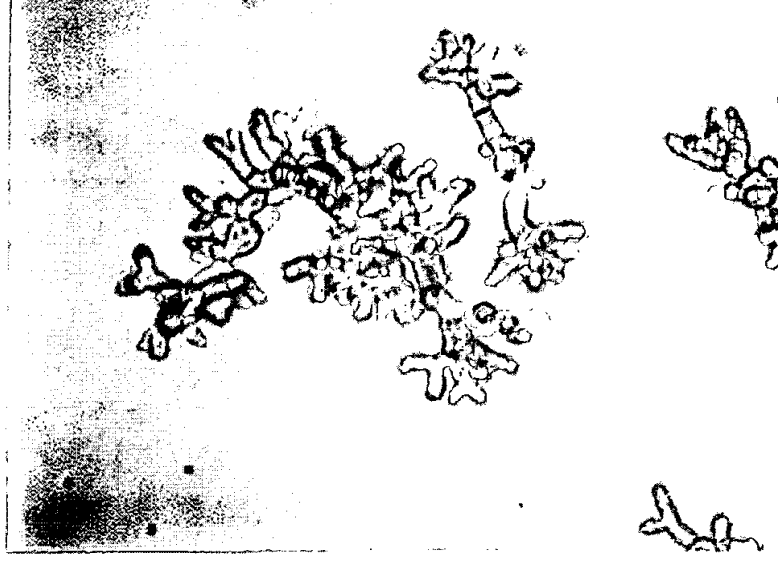


Fig 13B

REF ID: A445250

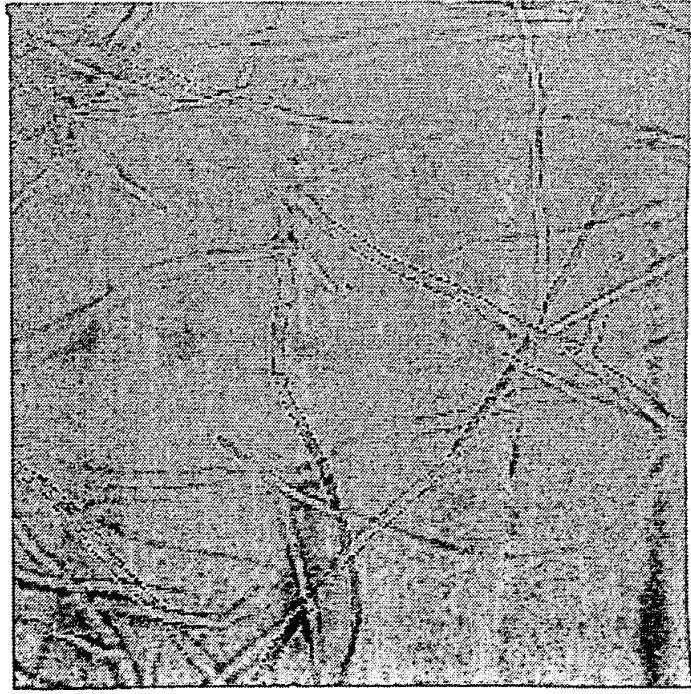


Fig. 14A

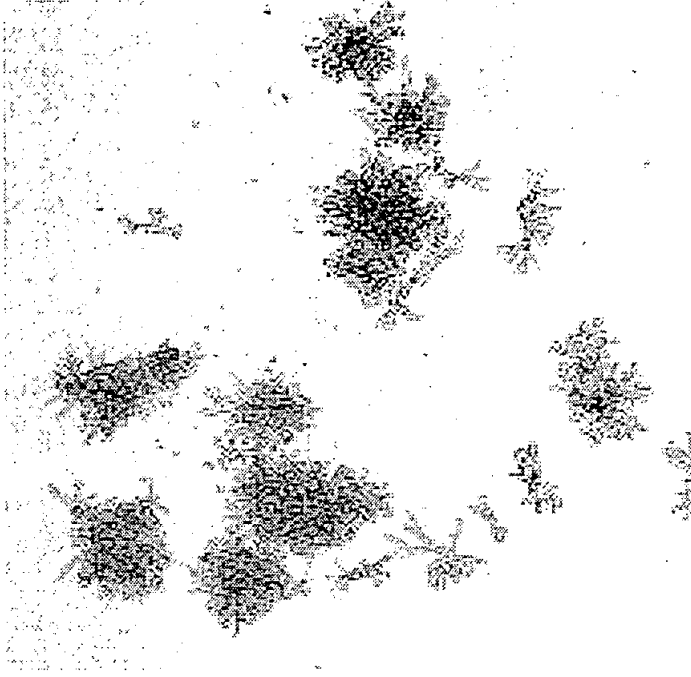


Fig. 14B

pyrE gene sequence

SEQ ID NO:1

Pyre/niger Length: 1578 March 9, 2001 09:28 Type: N Check: 2282

1 GGGTTAATGT GAAGGCGTTA GTGGTAATGT ATATTAATGG TGAGATGGGC
51 TTTGATTGGG TTTAATTGGA ATCTGTATAT TTTCAGATGG AGTCAACTTT
101 TGAATGGCCA ATATATCCTC GGCGATACCG TCGGAGATAA GATAAGAATA
151 ATCGCACACT ATTCCCAAAG CATACTGGTA CATACTGCAT TCGGCTAGTG
201 CGGGGTGCTT ACCTCATCCA CCCGAATGAG CCCAACTTTT TTGTCTCAAT
251 CAATAATTGC ATCCAAATTC CCCC GCAACT TCCCCCTCCA ACCCCGTGTC
301 TATACCACTC CCTCCACACC CACACAATCA CAATGGCTCT CCCTGCCTAC
351 AAGACCGCCT TCCTGGAGTC TCTCGTCGGC CAACGTGCTG ACTTTCGGCA
401 CCTTCACCCT GAAGTCGGGT CGCCGTGCGT CACCCCTCCA ACACCGGCAT
451 TATCGCAATC GGAAGACTTA CCACTGTATA CAGACTCCCC CTACTTCTTC
501 AACGCCGGCA TCTTCAACAC CGCCTCTCTC CTCTCCGCCC TCTCCACCAT
551 GGCCACACACC ATCATCACCT TCCTCGCTGA GAACCCTTCC ATCCCCAAGC
601 CCGACGTCAT GCTTCGGGTA AAAAACCCCC TCTTTCCCCA ATACCCCACT
651 TCCACTCAAC AACCCATAAA TAACTAACAA AAACCCCTTA AACAGCCCCG
701 CATACAAAGG CATCCCCCTC GCGTGCGCCA CCCTCCTTGA ACTCAACCGC
751 ATCGACCCCG CCACCTGGGG CAGCGTGTCC TACAGCTACA ACCGCAAAGA
801 AGCCAAGGAT CACGGCGAAG GCGGCAACAT TGTCGGCGCC GCTCTGAAGG
851 GCAAGACCGT GCTTGTGATC GACGATGTCA TCACGGCCGG TACCGCCATG
901 CGTGAGACCC TCAACCTGGT CGCCAAGGAG GGCGGCAAGG TCGTCGGATT
951 CACTGTTGCT CTGACCGCT TGGAGAAGAT GCCCGGACCC AAGGACGAGA
1001 ACGGTGTCGA GGACGATAAG CCCAGAATGA GTGCTATGGG TCAGATCCGT
1051 AAGGAGTATG GTGTGCCAC GACGAGTATT GTTACTCTGG ATGATTTGAT
1101 CAAGTTGATG CAGGCGAAGG GCAATGAGGC CGATATGAAG CGGTTGGAGG
1151 AGTATAGGGC TAAGTATCAG GCTAGTGATT AGTCGGTTTC ATTGACCGAT

FIG. 15A

1201 TGTTTGGGTG GGTGTGAGAG GTTAGGTTAG GTTGTGGGCG TAGGAATGAA
 1251 AAGCTGTATA CATAGGGGCC TGAAGAGGTG CGTAGAGACG GTCGTGAGAT
 1301 GTTTTATGTC AAAATCTTGA ACAAATGACA CCTTAAAAAA GACCCCTTGG
 1351 TTTCAGCTGA ATTAGCCCGG AAAGATGCTC GGCACGCCAT GAGTCTAGCC
 1401 CACTCAGTGG GCACCCGTTT CCCACATTTG AAGTGGCCGA CGCTTATTTG
 1451 GCTGAGGCTG TGGCCTGGAA AGGCACTATG GCGTGCTGCG GTACAAGGCC
 1501 GGGGCTGGCG TACGAACCAC GACGCCCCGA GGGAACCTCT CGGTCTTACT
 1551 ACTACTATGT CCCCAGTTGA CCCCCCGA

SEQ ID NO:2

Translation of pyrE(1-1578)
 Universal code

1 GGGTTAATGTGAAGGCGTTAGTGGTAATGTATATTAATGGTGAGATGGGCTTTGATTGGG
 CCCAATTACACTTCCGCAATCACCATTACATATAATTACCACTCTACCCGAAACTAACCC
 1 G L M * R R * W * C I L M V R W A L I G
 1 G * C E G V S G N V Y * W * D G L * L G
 1 V N V K A L V V M Y I N G E M G F D W V
 61 TTAAATTGGAATCTGTATATTTTCAGATGGAGTCAACTTTTGAATGGCCAATATATCCTC
 AAATTAACCTTAGACATATAAAAGTCTACCTCAGTTGAAAACCTTACCGGTTATATAGGAG
 21 F N W N L Y I F R W S Q L L N G Q Y I L
 21 L I G I C I F S D G V N F * M A N I S S
 21 * L E S V Y F Q M E S T F E W P I Y P R
 121 GGCGATACCGTCGGAGATAAGATAAGAATAATCGCACACTATTCCCAAAGCATACTGGTA
 CCGCTATGGCAGCCTCTATTCTATTCTTATTAGCGTGTGATAAGGGTTTCGTATGACCAT
 41 G D T V G D K I R I I A H Y S Q S I L V
 41 A I P S E I R * E * S H T I P K A Y W Y
 41 R Y R R R * D K N N R T L F P K H T G T
 181 CATACTGCATTTCGGCTAGTGCGGGGTGCTTACCTCATCCACCCGAATGAGCCCACTTTT
 GTATGACGTAAGCCGATCACGCCCCACGAATGGAGTAGGTGGGCTTACTCGGGTTGAAAA
 61 H T A F G * C G V L T S S T R M S P T F
 61 I L H S A S A G C L P H P P E * A Q L F
 61 Y C I R L V R G A Y L I H P N E P N F F

FIG. 15B

241 TTGTCTCAATCAATAATTGCATCCAAATTCCCCGCAACTTCCCCCTCCAACCCCGTGT
 AACAGAGTTAGTTATTAACGTAGGTTTAAGGGGGCGTTGAAGGGGGAGGTTGGGGCAG

 81 L S Q S I I A S K F P R N F P L Q P R V
 81 C L N Q * L H P N S P A T S P S N P V S
 81 V S I N N C I Q I P P Q L P P P T P C L
 ?????????

 301 TATACCACTCCCTCCACACCCACACAATCACAATGGCTCTCCCTGCCTACAAGACCGCCT
 ATATGGTGAGGGAGGTGTGGGTGTGTTAGTGTTACCGAGAGGGACGGATGTTCTGGCGGA

 101 Y T T P S T P T Q S Q W L S L P T R P P
 101 I P L P P H P H N H N G S P C L Q D R L
 101 Y H S L H T H T I T M A L P A Y K T A F

 361 TCCTGGAGTCTCTCGTCGGCCAACTGCTGACTTTCGGCACCTTCACCCTGAAGTCGGGT
 AGGACCTCAGAGAGCAGCCGTTGCACGACTGAAAGCCGTGGAAGTGGGACTTCAGCCCA
 ?????????????????????
 121 S W S L S S A N V L T F G T F T L K S G
 121 P G V S R R P T C * L S A P S P * S R V
 121 L E S L V G Q R A D F R H L H P E V G S

 INTRON I
 421 CGCCGTGCGTCACCCCTCCAACACCGGCATTATCGCAATCGGAAGACTTACCACTGTATA
 GCGGCACGCAGTGGGGAGGTTGTGGCCGTAATAGCGTTAGCCTTCTGAATGGTGACATAT

 141 R R A S P L Q H R H Y R N R K T Y H C I
 141 A V R H P S N T G I I A I G R L T T V Y
 141 P C V T P P T P A L S Q S E D L P L Y T

 481 CAGACTCCCCCTACTTCTTCAACGCCGGCATCTTCAACACCGCCTCTCTCCTCTCCGCCC
 GTCTGAGGGGGATGAAGAAGTTGCGGCCGTAGAAGTTGTGGCGGAGAGAGGAGAGGCGGG

 161 Q T P P T S S T P A S S T P P L S S P P
 161 R L P L L L Q R R H L Q H R L S P L R P
 161 D S P Y F F N A G I F N T A S L L S A L

 NcoI
 541 TCTCCACCATGGCCACACCATCATCACCTTCCTCGCTGAGAACCCTTCCATCCCCAAGC
 AGAGGTGGTACCGGGTGTGGTAGTAGTGGAAGGAGCGACTCTTGGAAGGTAGGGGTTCCG

 181 S P P W P T P S S P S S L R T L P S P S
 181 L H H G P H H H L P R * E P F H P Q A
 181 S T M A H T I I T F L A E N P S I P K P
 ?????????? INTRON II

 601 CCGACGTCATGCTTCGGGTAAAAAACCCCTCTTTCCCCAATACCCCACTTCCACTCAAC
 GGCTGCAGTACGAAGCCCATTTTTTGGGGGAGAAAGGGTTATGGGGTGAAGGTGAGTTG

 201 P T S C F G * K T P S F P N T P L P L N
 201 R R H A S G K K P P L S P I P H F H S T
 201 D V M L R V K N P L F P Q Y P T S T Q Q

FIG. 15C

661 AACCCATAAATAACTAACAAAAACCCCTAAACAGCCCCGCATACAAAGGCATCCCCCTC
TTGGGTATTTATTGATTGTTTTTGGGGGATTGTGCGGGGCGTATGTTTCCGTAGGGGGAG

221 N P * I T N K N P L N S P A Y K G I P L
221 T H K * L T K T P * T A P H T K A S P S
221 P I N N * Q K P P K Q P R I Q R H P P R

721 GCGTGCGCCACCCTCCTTGAACCTCAACCGCATCGACCCCGCCACCTGGGGCAGCGTGTCC
CGCACGCGGTGGGAGGAACCTTGAGTTGGCGTAGCTGGGGCGGTGGACCCCGTCGCACAGG

241 A C A T L L E L N R I D P A T W G S V S
241 R A P P S L N S T A S T P P P G A A C P
241 V R H P P * T Q P H R P R H L G Q R V L

781 TACAGCTACAACCGCAAAGAAGCCAAGGATCACGGCGAAGGCGGCAACATTGTGCGCGCC
ATGTGCGATGTTGGCGTTTCTTCGGTTCCTAGTGCCGCTTCCGCCGTTGTAACAGCCGCGG

261 Y S Y N R K E A K D H G E G G N I V G A
261 T A T T A K K P R I T A K A A T L S A P
261 Q L Q P Q R S Q G S R R R R Q H C R R R

841 GCTCTGAAGGGCAAGACCGTGCTTGTGATCGACGATGTCATCACGGCCGGTACCGCCATG
CGAGACTTCCCGTTCTGGCACGAACACTAGCTGCTACAGTAGTGCCGGCCATGGCGGTAC

281 A L K G K T V L V I D D V I T A G T A M
281 L * R A R P C L * S T M S S R P V P P C
281 S E G Q D R A C D R R C H H G R Y R H A

901 CGTGAGACCCTCAACCTGGTCGCCAAGGAGGGCGGCAAGGTCGTGCGATTCACTGTTGCT
GCACCTCTGGGAGTTGGACCAGCGGTTCTCCCGCCGTTCCAGCAGCCTAAGTGACAACGA

301 R E T L N L V A K E G G K V V G F T V A
301 V R P S T W S P R A A R S S D S L L L
301 * D P Q P G R Q G G R Q G R R I H C C S

961 CTGGACCGCTTGGAGAAGATGCCCCGACCCAAGGACGAGAACGGTGTGCGAGGACGATAAG
GACCTGGCGAACCTCTTCTACGGGCCTGGGTTCTGCTCTTGCCACAGCTCCTGCTATTC

321 L D R L E K M P G P K D E N G V E D D K
321 W T A W R R C P D P R T R T V S R T I S
321 G P L G E D A R T Q G R E R C R G R * A

1021 CCCAGAATGAGTGCTATGGGTGAGATCCGTAAGGAGTATGGTGTGCCCACGACGAGTATT
GGGTCTTACTCACGATAACCCAGTCTAGGCATTCCTCATACCACAGGGTGCTGCTCATAA

341 P R M S A M G Q I R K E Y G V P T T S I
341 P E * V L W V R S V R S M V C P R R V L
341 Q N E C Y G S D P * G V W C A H D E Y C

FIG. 15D

1081 GTTACTCTGGATGATTTGATCAAGTTGATGCAGGCGAAGGGCAATGAGGCCGATATGAAG
CAATGAGACCTACTAACTAGTTCAACTACGTCCGCTTCCCGTTACTCCGGCTATACTTC

361 V T L D D L I K L M Q A K G N E A D M K
361 L L W M I * S S * C R R R A M R P I * S
361 Y S G * F D Q V D A G E G Q * G R Y E A

1141 CGGTTGGAGGAGTATAGGGCTAAGTATCAGGCTAGTGATTAGTCGGTTTCATTGACCGAT
GCCAACCTCCTCATATCCCGATTATAGTCCGATCACTAATCAGCCAAAGTAACTGGCTA

381 R L E E Y R A K Y Q A S D * S V S L T D
381 G W R S I G L S I R L V I S R F H * P I
381 V G G V * G * V S G * * L V G F I D R L

1201 TGTTTGGGTGGGTGTGAGAGGTTAGGTTAGGTTGTGGGCGTAGGAATGAAAAGCTGTATA
ACAAACCCACCCACACTCTCCAATCCAATCCAACACCCGCATCCTTACTTTTCGACATAT

401 C L G G C E R L G * V V G V G M K S C I
401 V W V G V R G * V R L W A * E * K A V Y
401 F G W V * E V R L G C G R R N E K L Y T

1261 CATAGGGCCTGAAGAGGTGCGTAGAGACGGTCGTGAGATGTTTTATGTCAAAATCTTGA
GTATCCCCGGACTTCTCCACGCATCTCTGCCAGCACTCTACAAAATACAGTTTTAGAACT

421 H R G L K R C V E T V V R C F M S K S *
421 I G A * R G A * R R S * D V L C Q N L E
421 * G P E E V R R D G R E M F Y V K I L N

1321 ACAAATGACACCTTAAAAAGACCCCTTGTTTTCAGCTGAATTAGCCCGGAAAGATGCTC
TGTTTACTGTGGAATTTTTTCTGGGGAACCAAAGTCGACTTAATCGGGCCTTTCTACGAG

441 T N D T L K K T P W F Q L N * P G K M L
441 Q M T P * K R P L G F S * I S P E R C S
441 K * H L K K D P L V S A E L A R K D A R

1381 GGCACGCCATGAGTCTAGCCCACTCAGTGGGCACCCGTTTCCCACATTTGAAGTGGCCGA
CCGTGCGGTACTCAGATCGGGTGAGTCACCCGTGGGCAAAGGTGTAAACTTCACCGGCT

461 G T P * V * P T Q W A P V S H I * S G R
461 A R H E S S P L S G H P F P T F E V A D
461 H A M S L A H S V G T R F P H L K W P T

1441 CGCTTATTTGGCTGAGGCTGTGGCCTGGAAAGGCACTATGGCGTGCTGCGGTACAAGGCC
GCGAATAAACCGACTCCGACACCGGACCTTTCCGTGATACCGCACGACGCCATGTTCCGG

481 R L F G * G C G L E R H Y G V L R Y K A
481 A Y L A E A V A W K G T M A C C G T R P
481 L I W L R L W P G K A L W R A A V Q G R

FIG. 15E

